

## WEST Search History





DATE: Friday, September 16, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L32	L8 and L30	6
<input type="checkbox"/>	L31	L30 and L21	38
<input type="checkbox"/>	L30	(514/2)![CCLS]	6927
<input type="checkbox"/>	L29	(514)![CCLS]	0
<input type="checkbox"/>	L28	20020119129.pn.	1
<input type="checkbox"/>	L27	6093565.pn.	1
<input type="checkbox"/>	L26	6242587.pn.	1
<input type="checkbox"/>	L25	L24 and L17	6
<input type="checkbox"/>	L24	L23 or L9	161
<input type="checkbox"/>	L23	L4.ti.	38
<input type="checkbox"/>	L22	L9 and L17	6
<input type="checkbox"/>	L21	L20 and L17	7004
<input type="checkbox"/>	L20	cnB or (CN with beta) or (cn with B) canB or (can with b)	426576
<input type="checkbox"/>	L19	cnB or (CN with beta) or canB or (can with b)	426614
<input type="checkbox"/>	L18	L17 and L4	254
<input type="checkbox"/>	L17	L12 or L13 or L14 or L15 or L16	66807
<input type="checkbox"/>	L16	chen.in.	46722
<input type="checkbox"/>	L15	lian.in.	738
<input type="checkbox"/>	L14	gao.in.	2754
<input type="checkbox"/>	L13	yan.in.	4724
<input type="checkbox"/>	L12	wei.in.	15637
<input type="checkbox"/>	L11	L10 not @ay>1998	19
<input type="checkbox"/>	L10	L9 and L5	88
<input type="checkbox"/>	L9	L7 or L8	161
<input type="checkbox"/>	L8	L4.ab.	81
<input type="checkbox"/>	L7	L4.clm.	113
<input type="checkbox"/>	L6	L5 and L4	1221
<input type="checkbox"/>	L5	cancer\$ or tumor\$ or neoplas\$	172177
<input type="checkbox"/>	L4	calcineurin	1588
<input type="checkbox"/>	L3	L2 or L1	2
<input type="checkbox"/>	L2	6093565.pn.	1

☐ L1 6242587.pn.

1

END OF SEARCH HISTORY

OM protein - protein search, using sw model

Run on: August 30, 2005, 00:08:09 ; Search time 164 Seconds  
(without alignments)  
398.552 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCVVGGGLDIHKKMVVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	870	100.0	169	7	ADE55926	Ade55926 Rat Prote
2	870	100.0	169	7	ADE55928	Ade55928 Human Pro
3	870	100.0	170	2	AAW64200	Aaw64200 Human cal
4	870	100.0	170	3	AAB09978	Aab09978 Human HCN
5	870	100.0	170	8	ADI27357	Adi27357 Human cal
6	762	87.6	170	4	ABB60493	Abb60493 Drosophil
7	739	84.9	162	4	ABB65554	Abb65554 Drosophil
8	733	84.3	170	4	AAO14411	Aao14411 Calcineur
9	733	84.3	173	4	AAB64410	Aab64410 Amino aci

10	733	84.3	173	6	ADA55632	Ada55632	Human	pro
11	733	84.3	187	4	AAU87327	Aau87327	Novel	cen
12	733	84.3	187	8	ADI54642	Adi54642	Novel	hum
13	733	84.3	189	4	AAM95239	Aam95239	Human	rep
14	733	84.3	189	4	AAM43639	Aam43639	Human	pol
15	733	84.3	189	4	AAM43564	Aam43564	Human	pol
16	733	84.3	189	4	AAU19951	Aau19951	Novel	hum
17	733	84.3	189	4	ABB95936	Abb95936	Human	tes
18	733	84.3	189	4	AAU87615	Aau87615	Novel	cen
19	733	84.3	189	8	ADI54930	Adi54930	Novel	hum
20	733	84.3	189	8	ADM24660	Adm24660	Human	PRO
21	733	84.3	189	8	ADM24585	Adm24585	Human	PRO
22	728	83.7	170	3	AAB09977	Aab09977	Human	CNB
23	501	57.6	197	8	ADS24073	Ads24073	Bacterial	
24	496	57.0	175	2	AAU00881	Aay00881	Calcineur	
25	496	57.0	175	8	ADS43790	Ads43790	Bacterial	
26	429.5	49.4	195	8	ADS44352	Ads44352	Bacterial	
27	429	49.3	185	8	ADN21422	Adn21422	Bacterial	
28	393	45.2	90	3	AAG02990	Aag02990	Human	sec
29	373.5	42.9	178	3	AAU77951	Aay77951	A. thalia	
30	340.5	39.1	195	6	ABG74662	Abg74662	Murine	Ca
31	337.5	38.8	194	6	ABG74856	Abg74856	Human	cal
32	337.5	38.8	194	7	ADD46021	Add46021	Human	Pro
33	337.5	38.8	194	7	ADE59921	Ade59921	Human	Pro
34	337.5	38.8	194	7	ADE61228	Ade61228	Human	Pro
35	337.5	38.8	194	7	ADE59917	Ade59917	Human	Pro
36	337.5	38.8	195	6	ABG74661	Abg74661	Human	Ca2
37	337.5	38.8	195	6	ABU89717	Abu89717	Protein	d
38	321.5	37.0	189	4	ABB58936	Abb58936	Drosophil	
39	316.5	36.4	213	8	ADN23634	Adn23634	Bacterial	
40	303.5	34.9	195	8	ADN23801	Adn23801	Bacterial	
41	292	33.6	207	4	AAM43642	Aam43642	Human	pol
42	292	33.6	207	4	AAU19948	Aau19948	Novel	hum
43	292	33.6	207	4	AAU87620	Aau87620	Novel	cen
44	292	33.6	207	8	ADI54935	Adi54935	Novel	hum
45	292	33.6	207	8	ADM24663	Adm24663	Human	PRO

# ALIGNMENTS

## RESULT 1

ADE55926

ID ADE55926 standard; protein; 169 AA.

XX

AC ADE55926;

XX

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein P06705, SEQ ID NO 1760.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; P06705.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 169 AA;  
  
 Query Match 100.0%; Score 870; DB 7; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-83;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 60

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Db          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60

Qy          61 FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFQAFRIYDMDKDGYSISNGELFQVLKMMVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFQAFRIYDMDKDGYSISNGELFQVLKMMVG 120

Qy          121 NNLKDTQLQQIVDKTIINADKGDGRISFEEFCVVGGGLDIHKKMVVDV 169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 NNLKDTQLQQIVDKTIINADKGDGRISFEEFCVVGGGLDIHKKMVVDV 169

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RESULT 2

ADE55928

```

ID  ADE55928 standard; protein; 169 AA.
XX
AC  ADE55928;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Human Protein P06705, SEQ ID NO 1762.
XX
KW  Human; pain; neuronal tissue; gene therapy;
KW  spinal segmental nerve injury; chronic constriction injury; CCI;
KW  spared nerve injury; SNI; Chung.
XX
OS  Homo sapiens.
XX
PN  WO2003016475-A2.
XX
PD  27-FEB-2003.
XX
PF  14-AUG-2002; 2002WO-US025765.
XX
PR  14-AUG-2001; 2001US-0312147P.
PR  01-NOV-2001; 2001US-0346382P.
PR  26-NOV-2001; 2001US-0333347P.
XX
PA  (GEHO ) GEN HOSPITAL CORP.
PA  (FARB ) BAYER AG.
XX
PI  Woolf C, D'urso D, Befort K, Costigan M;
XX
DR  WPI; 2003-268312/26.
DR  GENBANK; P06705.
XX
PT  New composition comprising two or more isolated polypeptides, useful for
PT  preparing a medicament for treating pain in an animal.
XX
PS  Claim 1; Page; 1017pp; English.
XX
CC  The invention discloses a composition comprising two or more isolated rat
CC  or human polynucleotides or a polynucleotide which represents a fragment,
CC  derivative or allelic variation of the nucleic acid sequence. Also
CC  claimed are a vector comprising the novel polynucleotide, a host cell
CC  comprising the vector, a method for identifying a nucleotide sequence
CC  which is differentially regulated in an animal subjected to pain and a

```

CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 169 AA;

Query Match 100.0%; Score 870; DB 7; Length 169;

Best Local Similarity 100.0%; Pred. No. 7.8e-83;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADEIKRLGKRFFKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI	60
Db	1	GNEASYPLEMCSHFDADEIKRLGKRFFKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI	60
Qy	61	FDTDGNGEVDKFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYSNGELFQVLKMMVG	120
Db	61	FDTDGNGEVDKFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYSNGELFQVLKMMVG	120
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV	169
Db	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV	169

# RESULT 3

AAW64200

ID AAW64200 standard; protein; 170 AA.

XX

AC AAW64200;

XX

DT 09-NOV-1998 (first entry)

XX

DE Human calcineurin.

XX

KW Calcineurin; interferon receptor 1 binding protein; IR1B1; human.

XX

OS Homo sapiens.

XX

PN WO9831796-A1.

XX

PD 23-JUL-1998.  
 XX  
 PF 15-JAN-1998; 98WO-US000671.  
 XX  
 PR 15-JAN-1997; 97US-0035636P.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (MCIN/) MCINNIS P A.  
 XX  
 PI Revel M, Abramovitch C, Chebath JE;  
 XX  
 DR WPI; 1998-414096/35.  
 XX  
 PT New isolated interferon receptor binding proteins - used to develop  
 PT products for modulating sensitivity to interferon, e.g. in the treatment  
 PT of tumours or for prolonging graft survival.  
 XX  
 PS Example 2; Page 35-36; 64pp; English.  
 XX  
 CC This polypeptide comprises the human calcium-binding protein, calcineurin  
 CC -beta. A novel interferon receptor binding protein, IR1B1 (see AAW64199),  
 CC of the invention shows marked homology, e.g. calcium binding sites (E-F  
 CC handles), to calcineurin-beta; amino acid residues 50-171 show 59.8%  
 CC similarity and 32.5% identity. IR1B1 polypeptides and polynucleotides can  
 CC be used to develop products for modulating sensitivity to interferon,  
 CC e.g. in cancer therapy and for prolonging graft survival  
 XX  
 SQ Sequence 170 AA;

Query Match 100.0%; Score 870; DB 2; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-83;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDI 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDI 61  
 Qy 61 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFQAFRIYDMDKDGYISNGELFQVLKMMVG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 62 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFQAFRIYDMDKDGYISNGELFQVLKMMVG 121  
 Qy 121>NNLKDTQLQQIVDKTIINADKGDGGRISFEEFCAVVGGLDIHKKMVVDV 169  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 122>NNLKDTQLQQIVDKTIINADKGDGGRISFEEFCAVVGGLDIHKKMVVDV 170

RESULT 4  
 AAB09978

ID AAB09978 standard; protein; 170 AA.  
 XX  
 AC AAB09978;  
 XX  
 DT 19-OCT-2000 (first entry)  
 XX  
 DE Human HCNB protein.  
 XX  
 KW Human; CNBII; calcineurin B; regulatory subunit; HCNB.



XX  
 OS Homo sapiens.  
 XX  
 PN CN1249347-A.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 30-SEP-1998; 98CN-00121923.  
 XX  
 PR 30-SEP-1998; 98CN-00121923.  
 XX  
 PA (UYFU-) UNIV FUDAN.  
 XX  
 PI Yu L, Zhang H, Zhao Y;  
 XX  
 DR WPI; 2000-400725/35.  
 XX  
 PT Preparation of human calcineurin regulatory subunit and its coding  
 PT sequence.  
 XX  
 PS Disclosure; Fig 1; 18pp; Chinese.  
 XX  
 CC This invention describes the novel coding sequence of CNBII, a new member  
 CC of the human Calcineurin (CN) regulatory subunit Calcineurin B (CNB)  
 CC family. The polypeptide coded by said sequence is the homolog of human  
 CC CNB gene. The process relates to the polypeptide coded by the  
 CC polynucleotide, and the application and preparing process of said  
 CC polynucleotide and said polypeptide. This sequence represents the human  
 CC HCNB protein described in the method of the invention  
 XX  
 SQ Sequence 170 AA;

Query Match 100.0%; Score 870; DB 3; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-83;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADAIEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 GNEASYPLEMCSHFDADAIEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 61  
 Qy 61 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFARIYDMKDGYSISNGELFQVLKMMVG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 62 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFARIYDMKDGYSISNGELFQVLKMMVG 121  
 Qy 121 NNLKDTQLQQIVDKTIINADKGDGRISFEEFCVVGGGLDIHKKMVVDV 169  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 122 NNLKDTQLQQIVDKTIINADKGDGRISFEEFCVVGGGLDIHKKMVVDV 170

RESULT 5  
 ADI27357  
 ID ADI27357 standard; protein; 170 AA.  
 XX  
 AC ADI27357;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX

DE Human calcineurin regulatory subunit B, PPP3R1.  
XX  
KW Antisense; enzyme; calcineurin; regulatory subunit B; PPP3R1;  
KW immunosuppressive; nootropic; neuroprotective; protein phosphatase 3;  
KW autoimmune disorder; aberrant calcium signaling; neurological disease;  
KW Alzheimer's disease; human; gene.  
XX  
OS Homo sapiens.  
XX  
PN US2003236206-A1.  
XX  
PD 25-DEC-2003.  
XX  
PF 20-JUN-2002; 2002US-00177573.  
XX  
PR 20-JUN-2002; 2002US-00177573.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Freier SM;  
XX  
DR WPI; 2004-070608/07.  
DR N-PSDB; ADI27256.  
XX  
PT New antisense oligonucleotide compounds, useful for diagnosing,  
PT preventing and/or treating conditions with aberrant activity of PPP3R1,  
PT such as autoimmune disorders, aberrant calcium signaling and Alzheimer's  
PT disease.  
XX  
PS Disclosure; Page 31; 49pp; English.  
XX  
CC The invention relates to a new compound comprising 8-50 nucleobases in  
CC length targeted to a nucleic acid molecule encoding protein phosphatase 3  
CC (PPP3R1, the regulatory subunit of calcineurin), where the compound  
CC specifically hybridises with the nucleic acid and inhibits the expression  
CC of PPP3R1, i.e. is an antisense oligonucleotide (AO). Also included are a  
CC compound 8-50 nucleobases in length which specifically hybridises with at  
CC least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding PPP3R1, a method of inhibiting the expression of PPP3R1  
CC in cells or tissues (comprising contacting the cells or tissues with AO  
CC so that expression of PPP3R1 is inhibited), a method of treating an  
CC animal having a disease or condition associated with PPP3R1 (comprising  
CC administering AO to the animal so that expression of PPP3R1 is inhibited)  
CC and a method of screening for an antisense compound (comprising  
CC contacting a preferred target region of a nucleic acid molecule encoding  
CC PPP3R1 with one or more candidate antisense compounds having at least an  
CC 8-nucleobase portion which is complementary to the preferred target  
CC region, and selecting for one or more candidate antisense compounds which  
CC inhibit the expression of a nucleic acid encoding PPP3R1). The methods  
CC and compositions of the present invention are useful for the diagnosis,  
CC prevention and/or treatment of diseases or conditions associated with  
CC aberrant expression or activity of PPP3R1, such as autoimmune disorders,  
CC conditions having aberrant calcium signaling and neurological diseases  
CC like Alzheimer's disease. The present sequence is the PPP3R1 protein  
CC sequence.  
XX  
SQ Sequence 170 AA;

Query Match 100.0%; Score 870; DB 8; Length 170;  
Best Local Similarity 100.0%; Pred. No. 7.9e-83;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI	60
Db	2	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI	61
Qy	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKLQKLRFAFRIYMDKDGYSNGELFQVLKMMVG	120
Db	62	FDTDGNGEVDFKEFIEGVSQFSVKGDKLQKLRFAFRIYMDKDGYSNGELFQVLKMMVG	121
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV	169
Db	122	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV	170

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 00:10:19 ; Search time 39 Seconds  
(without alignments)  
416.939 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCVVGGLDIHKMVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID		Description
1	870	100.0	170	1	A33391		calcineurin regula
2	870	100.0	170	1	S34127		calcineurin regula
3	870	100.0	216	1	S42716		calcineurin regula
4	865	99.4	170	1	JC1220		calcineurin regula
5	784	90.1	170	2	JC7242		calcineurin regula
6	766	88.0	170	2	JC5174		calcineurin regula
7	762	87.6	170	2	A44307		calcineurin regula
8	704	80.9	369	2	T22708		hypothetical prote
9	702	80.7	179	2	JC1221		calcineurin regula
10	699	80.3	176	2	JQ1232		calcineurin regula
11	620	71.3	165	2	PS0261		calcineurin regula
12	528	60.7	174	2	T47245		calcineurin regula
13	496	57.0	175	2	JH0462		phosphoprotein pho

14	483	55.5	174	2	T41632	probable calcineur
15	316.5	36.4	213	2	T31775	hypothetical prote
16	303.5	34.9	195	2	T28047	hypothetical prote
17	255	29.3	311	2	T21563	hypothetical prote
18	233.5	26.8	150	2	T07122	calmodulin CAM5 -
19	233.5	26.8	151	2	A71409	calmodulin 8 [impo
20	230	26.4	591	2	S54788	calcium-stimulated
21	229.5	26.4	149	2	S35187	calmodulin 6 - Ara
22	228.5	26.3	149	1	S53006	calmodulin - leaf
23	228.5	26.3	149	1	MCPZDC	calmodulin - carro
24	228.5	26.3	149	1	S22503	calmodulin [simila
25	228.5	26.3	149	1	S22971	calmodulin - trum
26	228.5	26.3	149	1	S40301	calmodulin - red b
27	228.5	26.3	149	1	S70768	calmodulin CAM81 -
28	228.5	26.3	149	2	T47417	calmodulin 7 [simi
29	228.5	26.3	149	2	H84667	calmodulin (cam2)
30	227.5	26.1	149	1	MCBH	calmodulin - barle
31	227.5	26.1	149	1	MCWT	calmodulin - wheat
32	227.5	26.1	149	2	S24952	calmodulin 1 (clon
33	226.5	26.0	149	2	S58311	calmodulin - Biden
34	226.5	26.0	149	2	S60237	calmodulin PCM2/PC
35	225.5	25.9	149	1	MCZQF	calmodulin - malar
36	224.5	25.8	149	1	MCAA	calmodulin - alfal
37	224.5	25.8	149	2	S22860	calmodulin 2 (clon
38	223.5	25.7	149	1	I51202	calmodulin - duck
39	223.5	25.7	149	1	MCCH	calmodulin - chick
40	223.5	25.7	149	1	MCEE	calmodulin - elect
41	223.5	25.7	149	1	MCHU	calmodulin [valida
42	223.5	25.7	149	1	MCRT	calmodulin [valida
43	223.5	25.7	149	2	JC1305	calmodulin - Japan
44	223.5	25.7	149	2	I51402	calmodulin - Afric
45	223.5	25.7	149	2	S37707	calmodulin - mouse

#### ALIGNMENTS

##### RESULT 1

A33391

calcineurin regulatory chain - human

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Homo sapiens (man)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-Jul-2004

C;Accession: A33391

R;Guerini, D.; Krinks, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.

DNA 8, 675-682, 1989

A;Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding subunit of the Ca(2+)/calmodulin-stimulated protein phosphatase.

A;Reference number: A33391; MUID:90126237; PMID:2558868

A;Accession: A33391

A;Molecule type: mRNA

A;Residues: 1-170 <GUE>

A;Cross-references: UNIPROT:P06705; GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705

C;Genetics:

A;Gene: GDB:PPP3R1; CALNB

A;Cross-references: GDB:136804; OMIM:601302  
A;Map position: 2p16-2p15  
C;Complex: heterodimer with calcineurin catalytic chain  
C;Superfamily: calmodulin; calmodulin repeat homology  
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation  
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>  
F;18-49/Domain: calmodulin repeat homology <EF1>  
F;50-82/Domain: calmodulin repeat homology <EF2>  
F;87-119/Domain: calmodulin repeat homology <EF3>  
F;128-160/Domain: calmodulin repeat homology <EF4>  
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
F;3/Modified site: aspartic acid (Asn) #status predicted  
F;31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted  
F;63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted  
F;100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status predicted  
F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status predicted

Query Match 100.0%; Score 870; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 6e-56;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GNEASYPLEMC SHFDADEIKRLGKRFKKLDLDNSGSLSV EEFMSLP ELQQNPLVQRVIDI 60
      ||||||||||||||||||||||||||||||||||||||||||||
Db      2 GNEASYPLEMC SHFDADEIKRLGKRFKKLDLDNSGSLSV EEFMSLP ELQQNPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMKDG YISNGELFQVLKMMVG 120
      ||||||||||||||||||||||||||||||||||||||||||||
Db     62 FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMKDG YISNGELFQVLKMMVG 121

Qy    121>NNLKDTQLQQIVDKTIINADKDG DGRISFEEFC AVVGGLDIHKKMVVDV 169
      ||||||||||||||||||||||||||||||||||||||||||||
Db    122>NNLKDTQLQQIVDKTIINADKDG DGRISFEEFC AVVGGLDIHKKMVVDV 170

```

## RESULT 2

S34127

calcineurin regulatory chain [validated] - bovine

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: I45831; JT0297; S34127

R;Nargang, C.E.; Bottorff, D.A.; Adachi, K.

DNA Seq. 4, 313-318, 1994

A;Title: Isolation and characterization of a cDNA clone coding for the calcium-binding subunit of calcineurin from bovine brain: an identical amino acid sequence to the human protein.

A;Reference number: I45831; MUID:95102111; PMID:7803816

A;Accession: I45831

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-170 <NA2>  
A;Cross-references: UNIPROT:P06705; EMBL:X71666; NID:g312968; PIDN:CAA50659.1; PID:g312969  
R;Aitken, A.; Klee, C.B.; Cohen, P.  
Eur. J. Biochem. 139, 663-671, 1984  
A;Title: The structure of the B subunit of calcineurin.  
A;Reference number: JT0297; MUID:84132092; PMID:6321184  
A;Accession: JT0297  
A;Molecule type: protein  
A;Residues: 2-11,'M',13-153,'S',155-169 <AIT>  
R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sintchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Fleming, M.A.; Caron, P.R.; Hsiao, K.; Navia, M.A.  
submitted to the Brookhaven Protein Data Bank, August 1996  
A;Reference number: A66708; PDB:1TCO  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 2-170  
R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sintchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Fleming, M.A.; Caron, P.R.; Hsiao, K.; Navia, M.A.  
Cell 82, 507-522, 1995  
A;Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FKBP12-FK506 complex.  
A;Reference number: A56967; MUID:95360994; PMID:7543369  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
C;Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)  
C;Superfamily: calmodulin; calmodulin repeat homology  
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation  
F;2-170/Product: calcineurin regulatory chain #status experimental <MAT>  
F;18-49/Domain: calmodulin repeat homology <EF1>  
F;50-82/Domain: calmodulin repeat homology <EF2>  
F;87-119/Domain: calmodulin repeat homology <EF3>  
F;128-160/Domain: calmodulin repeat homology <EF4>  
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental  
F;3/Modified site: aspartic acid (Asn) #status predicted  
F;31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experimental  
F;63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experimental  
F;100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status experimental  
F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status experimental

Query Match 100.0%; Score 870; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 6e-56;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPQLQONPLVQRVIDI	60
Db	2	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPQLQONPLVQRVIDI	61
Qy	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG	120
Db	62	FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG	121
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV	169

Db

122>NNLKDTQLQQIVDKTIINADKGDGRISFEEFCAVVGGLDIHKKMVDV170

RESULT 3

S42716

calcineurin regulatory chain, long splice form - rat

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

N;Contains: calcineurin regulatory chain, short splice form

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: S42716; S42717

R;Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.

Biochim. Biophys. Acta 1217, 174-180, 1994

A;Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of Ca(2+)/calmodulin-dependent protein phosphatase (calcineurin B-alpha-2).

A;Reference number: S42716; MUID:94153993; PMID:8110831

A;Accession: S42716

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-216 <CHA1>

A;Cross-references: UNIPROT:P06705; EMBL:D14425; NID:g286205; PIDN:BAA03318.1; PID:g286206

A;Accession: S42717

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 'M',48-216 <CHA2>

A;Cross-references: EMBL:D14568; NID:g286255; PIDN:BAA03422.1; PID:g286256

C;Complex: heterodimer with calcineurin catalytic chain

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation

F;2-216/Product: calcineurin regulatory chain, long splice form #status predicted <MATL>

F;48-216/Product: calcineurin regulatory chain, short splice form #status predicted <MATS>

F;64-95/Domain: calmodulin repeat homology <EF1>

F;96-128/Domain: calmodulin repeat homology <EF2>

F;'M',48-216/Product: calcineurin regulatory chain, short splice form precursor #status predicted <PRES>

F;133-165/Domain: calmodulin repeat homology <EF3>

F;174-206/Domain: calmodulin repeat homology <EF4>

F;48/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

F;49/Modified site: aspartic acid (Asn) #status predicted

Query Match 100.0%; Score 870; DB 1; Length 216;

Best Local Similarity 100.0%; Pred. No. 7.8e-56;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVVEEFMSLPQLQONPLVQRVIDI 60

|||||

Db 48 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVVEEFMSLPQLQONPLVQRVIDI 107

Qy 61 FDTDGNGEVDFKEFIEGVSQFSVKGDKKEQKLRFARIYDMDKGYISNGELFQVLKMMVG 120

|||||



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Db          108 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYSISNGELFQVLKMMVG 167
Qy          121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          168 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 216

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RESULT 4

```

JC1220
calcineurin regulatory chain, brain - mouse
N;Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1;
phosphoprotein phosphatase chain B; protein phosphatase 2B
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC1220
R;Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A;Title: Structure and expression of two isoforms of the murine calmodulin-
dependent protein phosphatase regulatory subunit (calcineurin B).
A;Reference number: JC1220; MUID:92392379; PMID:1325794
A;Accession: JC1220
A;Molecule type: mRNA
A;Residues: 1-170 <UEK>
A;Cross-references: UNIPROT:Q63810; GB:S43864; NID:g255078; PIDN:AAB23171.1;
PID:g255079
A;Experimental source: brain
C;Comment: With calcineurin catalytic chain plays an important role in neural
and nonneural calcium-regulated signaling.
C;Genetics:
A;Gene: PP2B-beta-1
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand;
heterodimer; lipoprotein; myristylation
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status
predicted

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Query Match          99.4%; Score 865; DB 1; Length 170;
Best Local Similarity 99.4%; Pred. No. 1.4e-55;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GNEASYPLEMCSHFDADEIKRLGKRFFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 60
            |:||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSEASYPLEMCSHFDADEIKRLGKRFFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 61

Qy          61 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYSISNGELFQVLKMMVG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYSISNGELFQVLKMMVG 121

Qy          121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          122 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 170

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us-09-763-720-1.rup

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 00:08:59 ; Search time 171 Seconds  
(without alignments)  
506.090 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	870	100.0	169	1	CALB_BOVIN	P63099 bos taurus
2	870	100.0	169	1	CALB_HUMAN	P63098 homo sapien
3	870	100.0	169	1	CALB_RAT	P63100 rattus norv
4	870	100.0	170	2	Q66HZ0	Q66hz0 brachydanio
5	870	100.0	170	2	Q6DJJ3	Q6djj3 xenopus lae
6	870	100.0	170	2	Q6VN50	Q6vn50 xenopus tro
7	870	100.0	170	2	Q6VN51	Q6vn51 gallus gall
8	865	99.4	169	1	CALB_MOUSE	Q63810 mus musculu
9	860	98.9	170	2	Q7T063	Q7t063 xenopus lae
10	795	91.4	765	2	Q86YQ0	Q86yq0 homo sapien
11	791	90.9	170	2	Q9NkW7	Q9nkw7 patinopecte
12	769	88.4	169	2	Q7PQ91	Q7pq91 anopheles g
13	766	88.0	170	1	CALC_DROME	Q24214 drosophila
14	762	87.6	170	1	CALB_DROME	P48451 drosophila
15	762	87.6	170	2	Q95P81	Q95p81 bombyx mori
16	734.5	84.4	169	2	Q86H16	Q86h16 schistosoma
17	733	84.3	169	1	CALC_HUMAN	Q961z3 homo sapien
18	732.5	84.2	169	2	Q9NFN1	Q9nfn1 schistosoma
19	707	81.3	170	2	Q7YRC9	Q7yrc9 macaca mula
20	704	80.9	171	2	Q20804	Q20804 caenorhabdi
21	702	80.7	178	1	CALC_MOUSE	Q63811 mus musculu

					us-09-763-720-1.rup	
22	699	80.3	175	1	CALC_RAT	P28470 rattus norv
23	580	66.7	115	2	Q99LQ9	Q99lq9 mus musculu
24	544	62.5	173	1	CALB_YARLI	Q6cge6 yarrowia li
25	540.5	62.1	174	1	CALB_NEUCR	P87072 neurospora
26	528	60.7	175	1	CALB_CRYNE	Q9hde1 cryptococcu
27	517	59.4	177	1	CALB_NAEGR	P42322 naegleria g
28	499	57.4	175	1	CALB_ASHGO	Q757b7 ashbya goss
29	496	57.0	174	1	CALB_YEAST	P25296 saccharomyc
30	483	55.5	174	1	CALB_SCHPO	Q9uu93 schizosacch
31	483	55.5	175	1	CALB_CANGA	Q6flu4 candida gla
32	475	54.6	175	1	CALB_KLULA	Q874t7 kluyveromyc
33	469	53.9	174	1	CALB_DEBHA	Q6bws8 debaryomyc
34	451	51.8	177	2	Q8MQT6	Q8mqt6 toxoplasma
35	443.5	51.0	169	2	Q867N3	Q867n3 paramecium
36	442.5	50.9	180	2	Q9GP83	Q9gp83 dictyosteli
37	436	50.1	177	2	Q86RA7	Q86ra7 plasmodium
38	436	50.1	179	2	Q8IKV9	Q8ikv9 plasmodium
39	415.5	47.8	166	2	Q7RP38	Q7rp38 plasmodium
40	372	42.8	175	2	Q9U0X7	Q9u0x7 leishmania
41	340.5	39.1	194	1	CHP1_MOUSE	P61022 mus musculu
42	340.5	39.1	194	1	CHP1_RAT	P61023 rattus norv
43	338.5	38.9	193	2	Q6DK70	Q6dk70 xenopus tro
44	338.5	38.9	193	2	Q6DKL7	Q6dkl7 xenopus lae
45	337.5	38.8	194	1	CHP1_HUMAN	Q99653 homo sapien

#### ALIGNMENTS

##### RESULT 1

##### CALB\_BOVIN

ID CALB\_BOVIN STANDARD; PRT; 169 AA.  
AC P63099; P06705; P15117; Q08044;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory  
DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform  
DE 1).  
GN Name=PPP3R1; Synonyms=CNA2, CNB;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=95102111; PubMed=7803816;  
RA Nargang C.E., Bottorff D.A., Adachi K.;  
RT "Isolation and characterization of a cDNA clone coding for the  
RT calcium-binding subunit of calcineurin from bovine brain: an identical  
RT amino acid sequence to the human protein.";  
RL DNA Seq. 4:313-318(1994).  
RN [2]  
RP SEQUENCE OF 1-168.  
RC TISSUE=Brain;  
RX MEDLINE=84132092; PubMed=6321184;  
RA Aitken A., Klee C.B., Cohen P.;  
RT "The structure of the B subunit of calcineurin.";  
RL Eur. J. Biochem. 139:663-671(1984).  
RN [3]  
RP CALCIUM-BINDING DATA.

us-09-763-720-1.rup

RX MEDLINE=80101597; PubMed=293720;  
RA Klee C.B., Crouch T.H., Krinks M.H.;  
RT "Calcineurin: a calcium- and calmodulin-binding protein of the nervous  
RT system.";  
RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) IN COMPLEX WITH FKBP1A.  
RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;  
RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.,  
RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;  
RT "X-ray structure of calcineurin inhibited by the immunophilin-  
RT immunosuppressant FKBP12-FK506 complex.";  
RL Cell 82:507-522(1995).  
CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,  
CC calmodulin stimulated protein phosphatase. Confers calcium  
CC sensitivity.  
CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory  
CC subunit (B).  
CC -!- MISCELLANEOUS: This protein has four functional calcium-binding  
CC sites.  
CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X71666; CAA50659.1; -.  
DR PIR; I45831; S34127.  
DR PDB; 1TCO; X-ray; B=1-169.  
DR GO; GO:0005955; C:calcineurin complex; NAS.  
DR GO; GO:0005509; F:calcium ion binding; NAS.  
DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.  
DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF\_Hand\_like.  
DR InterPro; IPR008080; Parvalbumin.  
DR InterPro; IPR001125; Recoverin.  
DR Pfam; PF00036; efhand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR PROSITE; PS00018; EF\_HAND; 4.  
KW 3D-structure; Calcium-binding; Direct protein sequencing; Lipoprotein;  
KW Myristate; Repeat.  
FT INIT\_MET 0 0  
FT LIPID 1 1 N-myristoyl glycine.  
FT CA\_BIND 30 41 EF-hand 1.  
FT CA\_BIND 62 73 EF-hand 2.  
FT CA\_BIND 99 110 EF-hand 3.  
FT CA\_BIND 140 151 EF-hand 4.  
FT CONFLICT 11 11 C -> M (in Ref. 2).  
FT CONFLICT 153 153 C -> S (in Ref. 2).  
FT HELIX 16 29  
FT TURN 31 32  
FT STRAND 36 37  
FT HELIX 39 42  
FT TURN 43 44  
FT HELIX 46 49  
FT TURN 50 50  
FT TURN 52 53

## us-09-763-720-1.rup

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FT  HELIX      54      61
FT  TURN       63      64
FT  STRAND     69      70
FT  HELIX      71      78
FT  HELIX      79      81
FT  TURN       83      84
FT  HELIX      87      98
FT  TURN     100     101
FT  STRAND    105     106
FT  HELIX    108     119
FT  TURN    120     121
FT  HELIX    125     139
FT  TURN    141     142
FT  STRAND   147     148
FT  HELIX   149     156
FT  HELIX   157     159
FT  HELIX   161     164
SQ  SEQUENCE   169 AA;  19169 MW;  749141BD0434C90C CRC64;

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Query Match 100.0%; Score 870; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GNEASYPLEMCSHFDADKRLGKRFKKLDLNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60
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DB      1 GNEASYPLEMCSHFDADKRLGKRFKKLDLNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60

QY     61 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMKDGYSNGELFQVLKMMVG 120
      |||
DB     61 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMKDGYSNGELFQVLKMMVG 120

QY    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169
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DB    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169

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## RESULT 2

## CALB\_HUMAN

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ID  CALB_HUMAN  STANDARD;  PRT;  169 AA.
AC  P63098; P06705; P15117; Q08044;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE  subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE  1).
GN  Name=PPP3R1; Synonyms=CNA2, CNB;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90126237; PubMed=2558868;
RA  Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT  "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT  Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT  phosphatase.";
RL  DNA 8:675-682(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT  "Cloning of human full open reading frames in Gateway(TM) system entry

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vector (pDONR201).";  
 Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 [3]  
 SEQUENCE FROM N.A.  
 TISSUE=Blood;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [4]  
 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;  
 Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,  
 Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.,  
 Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,  
 Bacquet R., Villafranca J.E.;  
 "Crystal structures of human calcineurin and the human FKBP12-FK506-  
 calcineurin complex.";  
 Nature 378:641-644(1995).  
 [5]  
 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) IN COMPLEX WITH PPIA.  
 PubMed=12218175; DOI=10.1073/pnas.192206699;  
 Huai Q., Kim H.Y., Liu Y., Zhao Y., Mondragon A., Liu J.O., Ke H.;  
 "Crystal structure of calcineurin-cyclophilin-cyclosporin shows common  
 but distinct recognition of immunophilin-drug complexes.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:12037-12042(2002).  
 [6]  
 X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) IN COMPLEX WITH PPIA.  
 PubMed=12357034; DOI=10.1073/pnas.212504399;  
 Jin L., Harrison S.C.;  
 "Crystal structure of human calcineurin complexed with cyclosporin A  
 and human cyclophilin.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:13522-13526(2002).  
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,  
 CC calmodulin stimulated protein phosphatase. Confers calcium  
 CC sensitivity.  
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory  
 CC subunit (B).  
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding  
 CC sites.  
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
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DR EMBL; M30773; AAB08721.1; -.  
DR EMBL; BC027913; AAH27913.1; -.  
DR EMBL; CR456938; CAG33219.1; -.  
DR PIR; A33391; A33391.  
DR PDB; 1AUI; X-ray; B=1-169.  
DR PDB; 1M63; X-ray; B/F=1-169.  
DR PDB; 1MF8; X-ray; B=1-169.  
DR OGP; P63098; -.  
DR Genew; HGNC:9317; PPP3R1.  
DR MIM; 601302; -.  
DR GO; GO:0005955; C:calcineurin complex; NAS.  
DR GO; GO:0005509; F:calcium ion binding; NAS.  
DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.  
DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF\_Hand\_like.  
DR InterPro; IPR008080; Parvalbumin.  
DR InterPro; IPR001125; Recoverin.  
DR Pfam; PF00036; efhand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR PROSITE; PS00018; EF\_HAND; 4.  
KW 3D-structure; Calcium-binding; Lipoprotein; Myristate; Repeat.

FT	INIT_MET	0	0	By similarity.
FT	LIPID	1	1	N-myristoyl glycine (By similarity).
FT	CA_BIND	30	41	EF-hand 1.
FT	CA_BIND	62	73	EF-hand 2.
FT	CA_BIND	99	110	EF-hand 3.
FT	CA_BIND	140	151	EF-hand 4.
FT	HELIX	16	29	
FT	TURN	31	32	
FT	STRAND	36	37	
FT	HELIX	39	42	
FT	TURN	43	44	
FT	HELIX	46	49	
FT	TURN	50	50	
FT	TURN	52	53	
FT	HELIX	54	61	
FT	TURN	63	64	
FT	STRAND	69	70	
FT	HELIX	71	78	
FT	HELIX	79	81	
FT	TURN	83	84	
FT	HELIX	87	98	
FT	TURN	100	101	
FT	STRAND	105	106	
FT	HELIX	108	119	
FT	TURN	120	121	
FT	HELIX	125	139	
FT	TURN	141	142	
FT	STRAND	147	148	
FT	HELIX	149	156	
FT	HELIX	157	159	
FT	HELIX	161	164	

SQ SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;

Query Match 100.0%; Score 870; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-763-720-1.rup

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QY      1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDI 60
Db      1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDI 60

QY     61 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFQAFRIYDMKDGYSINGELFQVLKMMVG 120
Db     61 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFQAFRIYDMKDGYSINGELFQVLKMMVG 120

QY    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169
Db    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169

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RESULT 3

CALB\_RAT

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ID  CALB_RAT      STANDARD;      PRT;    169 AA.
AC  P63100; P06705; P15117; Q08044;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE  subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE  1).
GN  Name=Ppp3r1; Synonyms=Cna2, Cnb;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RC  STRAIN=Fischer;
RA  Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
RT  "Regulation of calcineurin phosphatase activity by the B subunit and
RT  carboxy-terminal inhibitory domains of the A subunit.";
RL  Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC  TISSUE=Brain, and Testis;
RX  MEDLINE=94153993; PubMed=8110831; DOI=10.1016/0167-4781(94)90031-0;
RA  Chang C.-D., Mukai H., Kuno T., Tanaka C.;
RT  "cDNA cloning of an alternatively spliced isoform of the regulatory
RT  subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin
RT  B alpha 2).";
RL  Biochim. Biophys. Acta 1217:174-180(1994).
CC  -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
CC  calmodulin stimulated protein phosphatase. Confers calcium
CC  sensitivity.
CC  -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
CC  subunit (B).
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1;
CC  IsoId=P63100-1, P06705-1;
CC  Sequence=Displayed;
CC  Name=2;
CC  IsoId=P63100-2, P06705-2;
CC  Sequence=VSP_000729;
CC  -!- TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC  -!- MISCELLANEOUS: This protein has four functional calcium-binding
CC  sites.
CC  -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC  -----

```



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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

Query Match 100.0%; Score 870; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADEIKRLGKRFKKLLDLSGSLSVEEFMSLPELQQNPLVQRVIDI	60
Db	1	GNEASYPLEMCSHFDADEIKRLGKRFKKLLDLSGSLSVEEFMSLPELQQNPLVQRVIDI	60
Qy	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKKEQKLRFARFIYDMDKDGYISNGELFQVLKMMVG	120
Db	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKKEQKLRFARFIYDMDKDGYISNGELFQVLKMMVG	120
Qy	121	NNLKDTQLQQIVDKTIINADKDGDDGRISFEEFCVVGGLDIHKKMVVDV	169
Db	121	NNLKDTQLQQIVDKTIINADKDGDDGRISFEEFCVVGGLDIHKKMVVDV	169

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ID   Q66HZ0                PRELIMINARY;          PRT;    170 AA.
AC   Q66HZ0;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Zgc:92169.
GN   Name=Zgc:92169;

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us-09-763-720-1.rup
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081617; AAH81617.1; -.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR008080; Parvalbumin.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.1e-52;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPQLQNPLVQRVIDI 60
|
Db 2 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPQLQNPLVQRVIDI 61

Qy 61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFARIYDMDKDGYISNGELFQVLKMMVG 120
|
Db 62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFARIYDMDKDGYISNGELFQVLKMMVG 121

Qy 121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVDV 169
|

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Db

122 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKMVDV 170

## RESULT 5

Q6DJJ3

ID Q6DJJ3 PRELIMINARY; PRT; 170 AA.  
 AC Q6DJJ3;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE MGC82148 protein.  
 GN Name=MGC82148;  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; *Xenopus*.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*  
 RT initiative."  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC075185; AAH75185.1; -.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR001751; CaBP\_S100.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF\_Hand\_like.  
 DR InterPro; IPR008080; Parvalbumin.  
 DR InterPro; IPR001125; Recoverin.  
 DR Pfam; PF00036; efhand; 4.

us-09-763-720-1.rup

DR PRINTS; PR01697; PARVALBUMIN.  
 DR PRINTS; PR00450; RECOVERIN.  
 DR ProDom; PD003407; CaBP\_S100; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR SMART; SM00054; EFh; 4.  
 DR PROSITE; PS00018; EF\_HAND; 4.  
 KW Calcium; Calcium-binding.  
 SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI 60  
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 Db 2 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI 61

QY 61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKLQKLRFAFRIYDMKDGYSINGELFQVLKMMVG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKLQKLRFAFRIYDMKDGYSINGELFQVLKMMVG 121

QY 121 NNKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKMMVVDV 169  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 122 NNKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKMMVVDV 170

RESULT 6  
 Q6VN50

ID Q6VN50 PRELIMINARY; PRT; 170 AA.  
 AC Q6VN50;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1  
 DE (Hypothetical protein MGC75600).  
 GN Name=MGC75600;  
 OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8364;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhou G., Li W., Yu L., Zhao S.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY336972; AAQ16148.1; -.  
DR EMBL; BC064854; AAH64854.1; -.  
DR HSSP; P02618; 1B8R.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR001751; CaBP\_S100.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF\_Hand\_like.  
DR InterPro; IPR008080; Parvalbumin.  
DR InterPro; IPR001125; Recoverin.  
DR Pfam; PF00036; efhand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR ProDom; PD003407; CaBP\_S100; 1.  
DR ProDom; PD000012; EF-hand; 2.  
DR SMART; SM00054; EFh; 4.  
DR PROSITE; PS00018; EF\_HAND; 4.  
KW Calcium; Calcium-binding; Hypothetical protein.  
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI	60
Db	2	GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI	61
Qy	61	FDTDGNGEVDFFEIEGVSVKGDKEQKLRFARIYDMKDGYISNGELFQVLKMMVG	120
Db	62	FDTDGNGEVDFFEIEGVSVKGDKEQKLRFARIYDMKDGYISNGELFQVLKMMVG	121
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEFFCAVVGGLDIHKKMVVDV	169
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RESULT 7  
Q6VN51

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Q6VN51 PRELIMINARY; PRT; 170 AA.
AC Q6VN51;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bursa;
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us-09-763-720-1.rup
RA   Zhou G., Li W., Yu L., Zhao S.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AY336970; AAQ16146.1; -.
DR   HSSP; P02618; 1B8R.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001751; CaBP_S100.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR010983; EF_Hand_like.
DR   InterPro; IPR008080; Parvalbumin.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR01697; PARVALBUMIN.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD003407; CaBP_S100; 1.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium; Calcium-binding.
SQ   SEQUENCE    170 AA;  19300 MW;  C904715DC0386056 CRC64;

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Query Match 100.0%; Score 870; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQQNPLVQRVIDI	60
Db	2	GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQQNPLVQRVIDI	61
Qy	61	FDTDGNGEVDKFKEFIEGVQSFSVKGDKEQKLRFARFIYDMDKDGYISNGELFQVLKMMVG	120
Db	62	FDTDGNGEVDKFKEFIEGVQSFSVKGDKEQKLRFARFIYDMDKDGYISNGELFQVLKMMVG	121
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEFFCAVVGGDIHKMKMVVDV	169
Db	122	NNLKDTQLQQIVDKTIINADKDGGRISFEFFCAVVGGDIHKMKMVVDV	170

us-09-763-720-1.ra1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2005, 00:18:39 ; Search time 43 Seconds  
(without alignments)  
293.388 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKMVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	870	100.0	169	3	US-08-720-625-4	Sequence 4, Appli
2	870	100.0	170	3	US-08-764-563-5	Sequence 5, Appli
3	702	80.7	179	3	US-08-764-563-4	Sequence 4, Appli
4	517	59.4	177	3	US-08-764-563-3	Sequence 3, Appli
5	496	57.0	174	1	US-08-328-322-17	Sequence 17, Appl
6	488	56.1	157	1	US-08-328-322-15	Sequence 15, Appl
7	469	53.9	204	4	US-09-248-796A-18332	Sequence 18332, A
8	393	45.2	90	4	US-09-513-999C-7071	Sequence 7071, Ap
9	321.5	37.0	233	4	US-09-270-767-42765	Sequence 42765, A
10	284	32.6	196	3	US-09-048-889-1	Sequence 1, Appli
11	242.5	27.9	145	3	US-08-720-625-5	Sequence 5, Appli
12	233.5	26.8	150	3	US-09-239-909-4	Sequence 4, Appli
13	225.5	25.9	149	3	US-08-963-409-3	Sequence 3, Appli
14	223.5	25.7	149	3	US-08-963-409-4	Sequence 4, Appli
15	223.5	25.7	149	3	US-08-641-873-20	Sequence 20, Appl
16	223.5	25.7	149	4	US-09-513-999C-7913	Sequence 7913, Ap
17	223.5	25.7	149	4	US-09-949-016-6770	Sequence 6770, Ap

				us-09-763-720-1.ra		
18	223.5	25.7	184	4	US-09-949-016-7507	Sequence 7507, Ap
19	222.5	25.6	416	4	US-09-989-025A-8	Sequence 8, Appli
20	221.5	25.5	150	3	US-09-239-909-2	Sequence 2, Appli
21	220.5	25.3	148	4	US-09-989-025A-4	Sequence 4, Appli
22	220.5	25.3	187	4	US-09-949-016-6721	Sequence 6721, Ap
23	215.5	24.8	142	1	US-07-951-715A-24	Sequence 24, Appl
24	215.5	24.8	142	2	US-08-459-448A-24	Sequence 24, Appl
25	215.5	24.8	142	3	US-08-459-595A-24	Sequence 24, Appl
26	215.5	24.8	142	3	US-08-459-504B-24	Sequence 24, Appl
27	215.5	24.8	142	3	US-08-459-444-24	Sequence 24, Appl
28	215.5	24.8	142	3	US-09-547-422-24	Sequence 24, Appl
29	215.5	24.8	142	4	US-09-988-462-24	Sequence 24, Appl
30	215	24.7	642	2	US-08-818-253-2	Sequence 2, Appli
31	215	24.7	642	3	US-08-818-252-2	Sequence 2, Appli
32	215	24.7	652	2	US-08-818-253-4	Sequence 4, Appli
33	215	24.7	652	3	US-08-818-252-4	Sequence 4, Appli
34	212	24.4	152	3	US-08-963-409-5	Sequence 5, Appli
35	212	24.4	152	4	US-09-949-016-6600	Sequence 6600, Ap
36	212	24.4	642	2	US-08-818-253-6	Sequence 6, Appli
37	212	24.4	642	3	US-08-818-252-6	Sequence 6, Appli
38	212	24.4	656	2	US-08-818-253-8	Sequence 8, Appli
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41	205	23.6	100	4	US-09-270-767-46741	Sequence 46741, A
42	205	23.6	163	2	US-08-698-805-8	Sequence 8, Appli
43	204.5	23.5	408	1	US-07-951-715A-21	Sequence 21, Appl
44	204.5	23.5	408	2	US-08-459-448A-21	Sequence 21, Appl
45	204.5	23.5	408	3	US-08-459-595A-21	Sequence 21, Appl

# ALIGNMENTS

## RESULT 1

US-08-720-625-4

; Sequence 4, Application US/08720625

; Patent No. 6242587

## GENERAL INFORMATION:

; APPLICANT: Naik, Ulhas P.

; APPLICANT: Parise, Leslie V.

; TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN

; NUMBER OF SEQUENCES: 10

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bell, Seltzer, Park & Gibson

; STREET: P.O. Drawer 34009

; CITY: Charlotte

; STATE: No. 6242587th Carolina

; COUNTRY: USA

; ZIP: 28234

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,625

; FILING DATE:

; CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

; NAME: Sibley, Kenneth D.

; REGISTRATION NUMBER: 31,665

; REFERENCE/DOCKET NUMBER: 5470-138

## TELECOMMUNICATION INFORMATION:



us-09-763-720-1.ra1

TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 169 amino acids  
 TYPE: amino acid  
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 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-720-625-4

Query Match 100.0%; Score 870; DB 3; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-81;  
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RESULT 2

US-08-764-563-5  
 ; Sequence 5, Application US/08764563  
 ; Patent No. 6093565  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Goli, Surya K.  
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/764,563  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0178 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166

us-09-763-720-1.ra1

; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 461682  
; US-08-764-563-5

Query Match 100.0%; Score 870; DB 3; Length 170;  
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Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKM	169
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us-09-763-720-1.rapb

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)  
407.390 Million cell updates/sec

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Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKMVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
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					Sequence 3, Appli

				us-09-763-720-1.rapb		
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3	733	84.3	170	15	US-10-239-572-2	Sequence 2, Appli
4	733	84.3	173	15	US-10-094-749-3200	Sequence 3200, Ap
5	733	84.3	187	11	US-09-764-875-845	Sequence 845, App
6	733	84.3	189	9	US-09-764-881-148	Sequence 148, App
7	733	84.3	189	10	US-09-764-891-3897	Sequence 3897, Ap
8	733	84.3	189	10	US-09-764-881-148	Sequence 148, App
9	733	84.3	189	11	US-09-764-875-1133	Sequence 1133, Ap
10	733	84.3	189	15	US-10-242-747-148	Sequence 148, App
11	733	84.3	189	15	US-10-158-057-242	Sequence 242, App
12	733	84.3	189	15	US-10-158-057-317	Sequence 317, App
13	531.5	61.1	174	16	US-10-425-115-330532	Sequence 330532,
14	501	57.6	197	15	US-10-369-493-13106	Sequence 13106, A
15	496	57.0	175	15	US-10-369-493-22220	Sequence 22220, A
16	429.5	49.4	195	15	US-10-369-493-22782	Sequence 22782, A
17	429	49.3	185	15	US-10-369-493-4075	Sequence 4075, Ap
18	373.5	42.9	178	14	US-10-342-224-54	Sequence 54, Appl
19	340.5	39.1	195	9	US-09-999-602-3	Sequence 3, Appli
20	340.5	39.1	195	17	US-10-482-838-18	Sequence 18, Appl
21	337.5	38.8	194	17	US-10-480-847-6	Sequence 6, Appli
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23	337.5	38.8	195	17	US-10-482-838-17	Sequence 17, Appl
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26	292	33.6	207	9	US-09-764-881-145	Sequence 145, App
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30	292	33.6	207	15	US-10-158-057-320	Sequence 320, App
31	291	33.4	196	17	US-10-482-838-9	Sequence 9, Appli
32	291	33.4	210	11	US-09-764-875-854	Sequence 854, App
33	289	33.2	199	15	US-10-276-774-2317	Sequence 2317, Ap
34	284	32.6	194	16	US-10-322-281-506	Sequence 506, App
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40	233	26.8	194	15	US-10-425-114-65892	Sequence 65892, A
41	232.5	26.7	150	16	US-10-739-930-8657	Sequence 8657, Ap
42	231.5	26.6	218	15	US-10-425-114-47771	Sequence 47771, A
43	230.5	26.5	171	16	US-10-437-963-185345	Sequence 185345,
44	230.5	26.5	174	15	US-10-425-114-59559	Sequence 59559, A
45	230.5	26.5	181	15	US-10-425-114-46972	Sequence 46972, A

#### ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/10109885
; Publication No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
METHODS OF
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL=14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01

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; us-09-763-720-1.rapb
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

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## RESULT 2

US-10-309-280-3

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; Sequence 3, Application US/10309280
; Publication No. US20030176678A1
; GENERAL INFORMATION:

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; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina

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; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
METHODS OF

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; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON

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; FILE REFERENCE: REVEL=14A

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; CURRENT APPLICATION NUMBER: US/10/309,280

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; CURRENT FILING DATE: 2002-12-04

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; PRIOR APPLICATION NUMBER: US/09/341,640

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; PRIOR FILING DATE: 1999-10-18

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; PRIOR APPLICATION NUMBER: PCT/US98/00671

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; PRIOR FILING DATE: 1998-01-15

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; PRIOR FILING DATE: 1997-01-15

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; NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 3

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; LENGTH: 170

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; TYPE: PRT

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; ORGANISM: Artificial Sequence

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; FEATURE:

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; OTHER INFORMATION: synthetic
US-10-309-280-3

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Best Local Similarity         100.0%; Pred. No. 3e-74;
Matches 169; Conservative     0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 FDTDGNGEVDFKEFIEGVSQFSVKGDKLRFQAFRIYDMKDGYSNGELFQVLKMMVG 120
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Qy      121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
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Db      122 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 170

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